

## RAW SEQUENCE LISTING

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Application Serial Number: 10/S16, 558  
Source: PCT  
Date Processed by STIC: 1-26-06

# ***ENTERED***



PCT

## RAW SEQUENCE LISTING

DATE: 01/26/2006

PATENT APPLICATION: US/10/516,558

TIME: 09:10:00

Input Set : A:\3190-070 Sequence Listing.txt

Output Set: N:\CRF4\01262006\J516558.raw

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3 <110> APPLICANT: Chano, Tokuhiko
4       Okabe, Hidetoshi
5       Ikegawa, Shiro
7 <120> TITLE OF INVENTION: RB1 gene induced protein (RB1CC1) and gene
9 <130> FILE REFERENCE: 3190-070
11 <140> CURRENT APPLICATION NUMBER: US 10/516,558
12 <141> CURRENT FILING DATE: 2004-11-30
14 <150> PRIOR APPLICATION NUMBER: PCT/JP03/00882
15 <151> PRIOR FILING DATE: 2003-01-30
17 <150> PRIOR APPLICATION NUMBER: JP P2002-161400
18 <151> PRIOR FILING DATE: 2002-06-03
20 <150> PRIOR APPLICATION NUMBER: JP P2002-214978
21 <151> PRIOR FILING DATE: 2002-07-24
23 <160> NUMBER OF SEQ ID NOS: 132
25 <170> SOFTWARE: PatentIn version 3.1
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 1594
29 <212> TYPE: PRT
30 <213> ORGANISM: Unknown
32 <220> FEATURE:
33 <223> OTHER INFORMATION: human RB1CC1
35 <400> SEQUENCE: 1
37 Met Lys Leu Tyr Val Phe Leu Val Asn Thr Gly Thr Thr Leu Thr Phe
38 1               5               10               15
41 Asp Thr Glu Leu Thr Val Gln Thr Val Ala Asp Leu Lys His Ala Ile
42           20           25           30
45 Gln Ser Lys Tyr Lys Ile Ala Ile Gln His Gln Val Leu Val Val Asn
46       35       40       45
49 Gly Gly Glu Cys Met Ala Ala Asp Arg Arg Val Cys Thr Tyr Ser Ala
50   50   55   60
53 Gly Thr Asp Thr Asn Pro Ile Phe Leu Phe Asn Lys Glu Met Ile Leu
54 65   70   75   80
57 Cys Asp Arg Pro Pro Ala Ile Pro Lys Thr Thr Phe Ser Thr Glu Asn
58       85       90       95
61 Asp Met Glu Ile Lys Val Glu Glu Ser Leu Met Met Pro Ala Val Phe
62   100   105   110
65 His Thr Val Ala Ser Arg Thr Gln Leu Ala Leu Glu Met Tyr Glu Val
66   115   120   125
69 Ala Lys Lys Leu Cys Ser Phe Cys Glu Gly Leu Val His Asp Glu His
70   130   135   140
73 Leu Gln His Gln Gly Trp Ala Ala Ile Met Ala Asn Leu Glu Asp Cys
74 145   150   155   160
77 Ser Asn Ser Tyr Gln Lys Leu Leu Phe Lys Phe Glu Ser Ile Tyr Ser

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78          165          170          175
81 Asn Tyr Leu Gln Ser Ile Glu Asp Ile Lys Leu Lys Leu Thr His Leu
82          180          185          190
85 Gly Thr Ala Val Ser Val Met Ala Lys Ile Pro Leu Leu Glu Cys Leu
86          195          200          205
89 Thr Arg His Ser Tyr Arg Glu Cys Leu Gly Arg Leu Asp Ser Leu Pro
90          210          215          220
93 Glu His Glu Asp Ser Glu Lys Ala Glu Thr Lys Arg Ser Thr Glu Leu
94 225          230          235          240
97 Val Leu Ser Pro Asp Met Pro Arg Thr Thr Asn Glu Ser Leu Leu Thr
98          245          250          255
101 Ser Phe Pro Lys Ser Val Glu His Val Ser Pro Asp Thr Ala Asp Ala
102          260          265          270
105 Glu Ser Gly Lys Glu Ile Arg Glu Ser Cys Gln Ser Thr Val His Gln
106          275          280          285
109 Gln Asp Glu Thr Thr Ile Asp Thr Lys Asp Gly Asp Leu Pro Phe Phe
110          290          295          300
113 Asn Val Ser Leu Leu Asp Trp Ile Asn Val Gln Asp Arg Pro Asn Asp
114 305          310          315          320
117 Val Glu Ser Leu Val Arg Lys Cys Phe Asp Ser Met Ser Arg Leu Asp
118          325          330          335
121 Pro Arg Ile Ile Arg Pro Phe Ile Ala Glu Cys Arg Gln Thr Ile Ala
122          340          345          350
125 Lys Leu Asp Asn Gln Asn Met Lys Ala Ile Lys Gly Leu Glu Asp Arg
126          355          360          365
128 Leu Tyr Ala Leu Asp Gln Met Ile Ala Ser Cys Gly Arg Leu Val Asn
129          370          375          380
132 Glu Gln Lys Glu Leu Ala Gln Gly Phe Leu Ala Asn Gln Lys Arg Ala
133 385          390          395          400
136 Glu Asn Leu Lys Asp Ala Ser Val Leu Pro Asp Leu Cys Leu Ser His
137          405          410          415
140 Ala Asn Gln Leu Met Ile Met Leu Gln Asn His Arg Lys Leu Leu Asp
141          420          425          430
144 Ile Lys Gln Lys Cys Thr Thr Ala Lys Gln Glu Leu Ala Asn Asn Leu
145          435          440          445
148 His Val Arg Leu Lys Trp Cys Cys Phe Val Met Leu His Ala Asp Gln
149          450          455          460
152 Asp Gly Glu Lys Leu Gln Ala Leu Leu Arg Leu Val Ile Glu Leu Leu
153 465          470          475          480
156 Glu Arg Val Lys Ile Val Glu Ala Leu Ser Thr Val Pro Gln Met Tyr
157          485          490          495
160 Cys Leu Ala Val Val Glu Val Val Arg Arg Lys Met Phe Ile Lys His
161          500          505          510
164 Tyr Arg Glu Trp Ala Gly Ala Leu Val Lys Asp Gly Lys Arg Leu Tyr
165          515          520          525
168 Glu Ala Glu Lys Ser Lys Arg Glu Ser Phe Gly Lys Leu Phe Arg Lys
169          530          535          540
172 Ser Phe Leu Arg Asn Arg Leu Phe Arg Gly Leu Asp Ser Trp Pro Pro
173 545          550          555          560

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176 Ser Phe Cys Thr Gln Lys Pro Arg Lys Phe Asp Cys Glu Leu Pro Asp
177          565          570          575
180 Ile Ser Leu Lys Asp Leu Gln Phe Leu Gln Ser Phe Cys Pro Ser Glu
181          580          585          590
184 Val Gln Pro Phe Leu Arg Val Pro Leu Leu Cys Asp Phe Glu Pro Leu
185          595          600          605
188 His Gln His Val Leu Ala Leu His Asn Leu Val Lys Ala Ala Gln Ser
189          610          615          620
191 Leu Asp Glu Met Ser Gln Thr Ile Thr Asp Leu Leu Ser Glu Gln Lys
192 625          630          635          640
195 Ala Ser Val Ser Gln Thr Ser Pro Gln Ser Ala Ser Ser Pro Arg Met
196          645          650          655
199 Glu Ser Thr Ala Gly Ile Thr Thr Thr Thr Ser Pro Arg Thr Pro Pro
200          660          665          670
203 Pro Leu Thr Val Gln Asp Pro Leu Cys Pro Ala Val Cys Pro Leu Glu
204          675          680          685
207 Glu Leu Ser Pro Asp Ser Ile Asp Ala His Thr Phe Asp Phe Glu Thr
208          690          695          700
211 Ile Pro His Pro Asn Ile Glu Gln Thr Ile His Gln Val Ser Leu Asp
212 705          710          715          720
215 Leu Asp Ser Leu Ala Glu Ser Pro Glu Ser Asp Phe Met Ser Ala Val
216          725          730          735
219 Asn Glu Phe Val Ile Glu Glu Asn Leu Ser Ser Pro Asn Pro Ile Ser
220          740          745          750
223 Asp Pro Gln Ser Pro Glu Met Met Val Glu Ser Leu Tyr Ser Ser Val
224          755          760          765
227 Ile Asn Ala Ile Asp Ser Arg Arg Met Gln Asp Thr Asn Val Cys Gly
228          770          775          780
231 Lys Glu Asp Phe Gly Asp His Thr Ser Leu Asn Val Gln Leu Glu Arg
232 785          790          795          800
235 Cys Arg Val Val Ala Gln Asp Ser His Phe Ser Ile Gln Thr Ile Lys
236          805          810          815
239 Glu Asp Leu Cys His Phe Arg Thr Phe Val Gln Lys Glu Gln Cys Asp
240          820          825          830
243 Phe Ser Asn Ser Leu Lys Cys Thr Ala Val Glu Ile Arg Asn Ile Ile
244          835          840          845
247 Glu Lys Val Lys Cys Ser Leu Glu Ile Thr Leu Lys Glu Lys His Gln
248          850          855          860
251 Lys Glu Leu Leu Ser Leu Lys Asn Glu Tyr Glu Gly Lys Leu Asp Gly
252 865          870          875          880
254 Leu Ile Lys Glu Thr Glu Glu Asn Glu Asn Lys Ile Lys Lys Leu Lys
255          885          890          895
258 Gly Glu Leu Val Cys Leu Glu Glu Val Leu Gln Asn Lys Asp Asn Glu
259          900          905          910
262 Phe Ala Leu Val Lys His Glu Lys Glu Ala Val Ile Cys Leu Gln Asn
263          915          920          925
266 Glu Lys Asp Gln Lys Leu Leu Glu Met Glu Asn Ile Met His Ser Gln
267          930          935          940
270 Asn Cys Glu Ile Lys Glu Leu Lys Gln Ser Arg Glu Ile Val Leu Glu

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271 945          950          955          960
274 Asp Leu Lys Lys Leu His Val Glu Asn Asp Glu Lys Leu Gln Leu Leu
275          965          970          975
278 Arg Ala Glu Leu Gln Ser Leu Glu Gln Ser His Leu Lys Glu Leu Glu
279          980          985          990
282 Asp Thr Leu Gln Val Arg His Ile Gln Glu Phe Glu Lys Val Met Thr
283          995          1000          1005
286 Asp His Arg Val Ser Leu Glu Glu Leu Lys Lys Glu Asn Gln Gln
287          1010          1015          1020
290 Ile Ile Asn Gln Ile Gln Glu Ser His Ala Glu Ile Ile Gln Glu
291          1025          1030          1035
294 Lys Glu Lys Gln Leu Gln Glu Leu Lys Leu Lys Val Ser Asp Leu
295          1040          1045          1050
298 Ser Asp Thr Arg Cys Lys Leu Glu Val Glu Leu Ala Leu Lys Glu
299          1055          1060          1065
302 Ala Glu Thr Asp Glu Ile Lys Ile Leu Leu Glu Glu Ser Arg Ala
303          1070          1075          1080
306 Gln Gln Lys Glu Thr Leu Lys Ser Leu Leu Glu Gln Glu Thr Glu
307          1085          1090          1095
310 Asn Leu Arg Thr Glu Ile Ser Lys Leu Asn Gln Lys Ile Gln Asp
311          1100          1105          1110
314 Asn Asn Glu Asn Tyr Gln Val Gly Leu Ala Glu Leu Arg Thr Leu
315          1115          1120          1125
317 Met Thr Ile Glu Lys Asp Gln Arg Ile Ser Glu Leu Ile Ser Arg
318          1130          1135          1140
321 His Glu Glu Glu Ser Asn Ile Leu Lys Ala Glu Leu Asn Lys Val
322          1145          1150          1155
325 Thr Ser Leu His Asn Gln Ala Phe Glu Ile Glu Lys Asn Leu Lys
326          1160          1165          1170
329 Glu Gln Ile Ile Glu Leu Gln Ser Lys Leu Asp Ser Glu Leu Ser
330          1175          1180          1185
333 Ala Leu Glu Arg Gln Lys Asp Glu Lys Ile Thr Gln Gln Glu Glu
334          1190          1195          1200
337 Lys Tyr Glu Ala Ile Ile Gln Asn Leu Glu Lys Asp Arg Gln Lys
338          1205          1210          1215
341 Leu Val Ser Ser Gln Glu Gln Asp Arg Glu Gln Leu Ile Gln Lys
342          1220          1225          1230
345 Leu Asn Cys Glu Lys Asp Glu Ala Ile Gln Thr Ala Leu Lys Glu
346          1235          1240          1245
349 Phe Lys Leu Glu Arg Glu Val Val Glu Lys Glu Leu Leu Glu Lys
350          1250          1255          1260
353 Val Lys His Leu Glu Asn Gln Ile Ala Lys Ser Pro Ala Ile Asp
354          1265          1270          1275
357 Ser Thr Arg Gly Asp Ser Ser Ser Leu Val Ala Glu Leu Gln Glu
358          1280          1285          1290
361 Lys Leu Gln Glu Glu Lys Ala Lys Phe Leu Glu Gln Leu Glu Glu
362          1295          1300          1305
365 Gln Glu Lys Arg Lys Asn Glu Glu Met Gln Asn Val Arg Thr Ser
366          1310          1315          1320

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```

369 Leu Ile Ala Glu Gln Gln Thr Asn Phe Asn Thr Val Leu Thr Arg
370      1325      1330      1335
373 Glu Lys Met Arg Lys Glu Asn Ile Ile Asn Asp Leu Ser Asp Lys
374      1340      1345      1350
377 Leu Lys Ser Thr Met Gln Gln Gln Glu Arg Asp Lys Asp Leu Ile
378      1355      1360      1365
381 Glu Ser Leu Ser Glu Asp Arg Ala Arg Leu Leu Glu Glu Lys Lys
382      1370      1375      1380
385 Lys Leu Glu Glu Glu Val Ser Lys Leu Arg Ser Ser Ser Phe Val
386      1385      1390      1395
389 Pro Ser Pro Tyr Val Ala Thr Ala Pro Glu Leu Tyr Gly Ala Cys
390      1400      1405      1410
393 Ala Pro Glu Leu Pro Gly Glu Ser Asp Arg Ser Ala Val Glu Thr
394      1415      1420      1425
397 Ala Asp Glu Gly Arg Val Asp Ser Ala Met Glu Thr Ser Met Met
398      1430      1435      1440
401 Ser Val Gln Glu Asn Ile His Met Leu Ser Glu Glu Lys Gln Arg
402      1445      1450      1455
405 Ile Met Leu Leu Glu Arg Thr Leu Gln Leu Lys Glu Glu Glu Asn
406      1460      1465      1470
409 Lys Arg Leu Asn Gln Arg Leu Met Ser Gln Ser Met Ser Ser Val
410      1475      1480      1485
413 Ser Ser Arg His Ser Glu Lys Ile Ala Ile Arg Asp Phe Gln Val
414      1490      1495      1500
417 Gly Asp Leu Val Leu Ile Ile Leu Asp Glu Arg His Asp Asn Tyr
418      1505      1510      1515
421 Val Leu Phe Thr Val Ser Pro Thr Leu Tyr Phe Leu His Ser Glu
422      1520      1525      1530
425 Ser Leu Pro Ala Leu Asp Leu Lys Pro Gly Glu Gly Ala Ser Gly
426      1535      1540      1545
429 Ala Ser Arg Arg Pro Trp Val Leu Gly Lys Val Met Glu Lys Glu
430      1550      1555      1560
433 Tyr Cys Gln Ala Lys Lys Ala Gln Asn Arg Phe Lys Val Pro Leu
434      1565      1570      1575
437 Gly Thr Lys Phe Tyr Arg Val Lys Ala Val Ser Trp Asn Lys Lys
438      1580      1585      1590
441 Val
446 <210> SEQ ID NO: 2
447 <211> LENGTH: 1588
448 <212> TYPE: PRT
449 <213> ORGANISM: Unknown
451 <220> FEATURE:
452 <223> OTHER INFORMATION: mouse Rb1cc1
454 <400> SEQUENCE: 2
456 Met Lys Leu Tyr Val Phe Leu Val Asn Thr Gly Thr Thr Leu Thr Phe
457 1      5      10      15
460 Asp Thr Glu Leu Thr Val Gln Thr Val Ala Asp Leu Lys His Ala Ile
461      20      25      30
464 Gln Ser Lys Tyr Lys Ile Ala Ile Gln His Gln Val Leu Val Val Asn

```

RAW SEQUENCE LISTING ERROR SUMMARY  
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,  
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30  
Seq#:31,32,33,34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54  
Seq#:55,56,57,58,59,60,61,62,63,64,65,66,67,68,69,70,71,72,73,74,75,76,77,78  
Seq#:79,80,81,82,83,84,85,86,87,88,89,90,91,92,93,94,95,96,97,98,99,100,101  
Seq#:102,103,104,105,106,107,108,109,110,111,112,113,114,115,116,117,118,119  
Seq#:120,121,122,123,124,125,126,127,128,129,130,131,132

**VERIFICATION SUMMARY**

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